



## **INTRODUCTION**

Advances in medical intervention provide a growing number of immunocompromised patients who are at risk from opportunistic fungal infection (*Coleman et al., 2005*) and now it is widely published and accepted that invasive fungal infections are a major cause of mortality and morbidity in the immunocompromised states such as some neutropenic patients with hematological malignancies, chemotherapy, organ transplantation, AIDS and other disease that can affect the immune system (*Newman et al., 2005*).

*Candida* and *Aspergillus* species account for the vast majority of fungal infections, but other less commonly recognized fungi can cause life- threatening infection in these hosts as well (*Segal and Minamoto, 2001*).

*Candida* species are the fourth most commonly encountered hospital acquired pathogens in blood stream infections and it is associated with mortality rates as high as 60% (*Nishikawa et al., 2003*).

So early initiation of antifungal therapy is paramount in reducing the high mortality rates associated with fungaemia and this is dependent on early detection of fungal infection (*Morace et al., 2003*).

The current “gold standard” for detection of systemic infection is blood culture, but this is believed to lack sensitivity and has been shown to be positive in less than 50% of patient with chronic disseminated candidiasis also it is time- consuming taking up to 3 weeks, and this is an unacceptable period for the treatment of fungaemia (*Einsele et al., 2003*).



This lack of reliable early diagnosis may lead to the unnecessary empirical treatment of patients who do not have fungal infection. The end result is unacceptable toxicity in many patients, massive expense and resistance to commonly used antifungal agents (*Mitchell, 2004*).

The accepted limitations associated with classic culture techniques for the diagnosis of invasive fungal infections have lead to the emergence of many non-culture-based methods, with superior sensitivities and quicker turn around times (*Widjojoatmodjo et al., 2003*).

Methods have been developed for the detection of both circulating antibodies and antigens, but the usefulness of antibody detection may be limited when the patients under investigation are immunosuppressed and or heavily colonized but uninfected (*Loeffler et al., 2003*).

Among the various antigens present in the blood of patients suffering from invasive fungal infection, carbohydrates, particularly cell wall components; are favored for the diagnosis of the infection. For the detection of *Candida*, the polysaccharide mannan is a major marker, as it contributes over 7% of the dry weight of the yeast *C. albicans*. It is non covalently bound to the cell wall and is extremely immunogenic (*Coleman et al., 2005*).

The use of PCR in the detection of systemic fungal infection has been extensively published and provides potential in terms of sensitivity and specificity. A range of PCR targets have been used including cytochrome P450 genes, heat shock protein genes and pH regulation genes, although primers that amplify the rRNA genes (18S, 28S and 5.8S rRNA genes) are the most frequently used due to their universal nature and large copy number (*Nishikawa et al., 2003*). A variety of post amplification methods have been used to exploit the variable regions



within the rRNA amplicons and identify the genus or species causing infection. These include nested PCR, restriction fragment length polymorphism (RFLP), PCR-enzyme-linked immunosorbent assay (ELISA), single strand confirmation polymorphism, hybridization with specific probes and sequencing, all of which increase complexity (*Loeffler et al, 2003*).

The major drawback with these techniques is that they require post amplification handling and so increase the time to result and more importantly, the chance of contamination (*Widjoatmodjo et al., 2003*).

The most promising PCR technique utilized fluorescently labeled specific probes and real-time PCR. This removes the need for post-amplification handling, reducing both turnaround time and the potential for contamination, and provides a species/ genus level of identification, depending on the design of the probe (*Einsele et al., 2003*).